To Process Replicate Data:

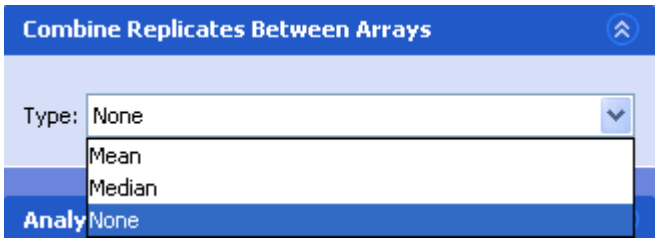
If you have more than one array for a particular sample (technical replicates), you can load these by adding additional **File** columns to the sample descriptor. For dye-swap experiments, see further below. The column header must be **File** suffixed with a number (e.g. File1, File2, File3, etc.). **File** without a numerical suffix can also be used for one of the columns:

File File1 File2 File3 File4…

Sample descriptor for Agilent samples with technical replicates:

Data Type:	Agilent FE			
Sample Name	File	File2	File3	Factor:Gender
sample 1	C:\BrainTumorProject\array1.txt	C:\BrainTumorProject\array11.txt	C:\BrainTumorProject\array31.txt	M
sample 2	C:\BrainTumorProject\array2.txt	C:\BrainTumorProject\array12.txt		F
sample 3	C:\BrainTumorProject\array3.txt	C:\BrainTumorProject\array13.txt		M

How the technical replicates are handled is determined by what settings are used for processing that data type within Nexus. **Combine Replicates Between Arrays** is a parameter that can be modified via the **Settings** window:



In the **Chromosome** view in the sample drill down, probes from each array will be displayed in a different color. The sample drill down shows the data prior to replicate combination operation so even if replicates between arrays were set to be combined during processing, the sample drill down will display the probes from each array for the sample. The probe color for each array depends on the column header:

File – blue
File1 – red
File2 – green
File3 – cyan
File4 – magenta
File5 – pink
File6 – orange
All others – gray

Please refer to the document specific for your data type for further information on how to load and process your data.

DYE-SWAP DATA

With dye swap experiments for two color arrays, two arrays are run for each sample where the dye used for the experimental and control samples is reversed on one array with respect to the other array. Additional **File** columns are added to the sample descriptor as described above. For analysis of dye swap data, the intensity ratio needs to be reversed for one of the arrays and Nexus needs to know which one to reverse. Ratio reversal is indicated by prefixing a minus sign to the column header:

File1 -File2

Data for the two arrays is combined to remove dye effects and then the aberrations are displayed. Any number of dye swap data can be added to each sample by adding additional columns and prefixing the column header with a minus sign for the array that needs to have its ratio reversed.

In the example below, **File** and **–File2** refer to a pair of dye swap experiments for the samples in the project.

Data Type:	Agilent FE			
Sample Name	File	-File2	Factor:Gender	Factor:Tumor Type
sample 1	C:\BrainTumorProject\array1.txt	C:\BrainTumorProject\array1R.txt	M	GBM
sample 2	C:\BrainTumorProject\array2.txt	C:\BrainTumorProject\array2R.txt	F	AOA
sample 3	C:\BrainTumorProject\array3.txt	C:\BrainTumorProject\array3R.txt	M	AOA

Please refer to the document specific for your data type for further information on how to load and process your data (you will have to use the sample descriptor method to load replicate data).

Please note that when editing files in Excel, starting a cell with an operator (e.g. minus sign) causes Excel to add and equal sign to the beginning of the cell. Nexus will be unable to load this file. So after creating the descriptor file, open it in Notepad or similar software and remove the equal sign if present before loading the descriptor into Nexus.